IN THE CLAIMS

Please amend the claims as follows:

4. (Amended) The method according to Claim 1, wherein said autogenous regulatory factor is a butyrolactone autogenous regulatory factor.

5. (Amended) The method according to Claim 1, wherein said autogenous regulatory factor is virginiae butanolide.

6. (Amended) The method according to Claim 1, wherein said gene expression inducing system is involved in a production of an antibiotic.

7. (Amended) The method according to Claim 1, wherein said gene expression inducing system is involved in a production of virginiamycin.

8. (Amended) The method according to Claim 1, wherein said repressor gene is a barA gene.

9. (Amended) The method according to Claim 1, wherein said repressor gene contains a region comprising a nucleotide sequence shown under SEQ ID NO:1.

10. (Amended) The method according to Claim 1, wherein said repressor gene contains a region coding for an amino acid sequence shown under SEQ ID NO:2.

11. (Amended) The method according to Claim 1, wherein a promoter for said repressor gene is a plant promotor.

13. (Amended) The method according to Claim 1, wherein a nucleotide sequence of said operator is derived from a barA, barB or barX gene.

14. (Amended) The method according to Claim 1, wherein a nucleotide sequence of said operator is BARE-1, BARE-2 or BARE-3.

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15. (Amended) The method according to Claim 1, wherein a nucleotide sequence of said operator is BARE-3.

16. (Amended) The method according to Claim 1, wherein the nucleotide sequence of said operator contains a region comprising a nucleotide sequence shown under SEQ ID NO:3.

17. (Amended) The method according to Claim 1, wherein a promoter for said gene placed under the control of the operator is a plant promoter.

19. (Amended) The method according to Claim 17, wherein said operator is disposed in at least one place in said plant promoter.

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20. (Amended) The method according to Claim 17, wherein said operator is disposed in at least one place in the vicinity of a site 3' downstream or in the vicinity of a site 5' upstream of a TATA box of said plant promoter.

21. (Amended) The method according to Claim 17, wherein said operator is disposed, together with the TATA box of said plant promoter, in a manner shown under any of SEQ ID NO:4 through SEQ ID NO:7.

22. (Amended) The method according to Claim 1, wherein said gene placed under the control of the operator is a gene capable of providing the plant with fertility.

23. (Amended) A plant transformed by the method according to Claim 1.

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24. (Amended) Tobacco (Nicotiana tabacum L.) transformed by the method according to Claim 1.

25. (Amended) A cultured plant cell transformed by the method according to Claim 1.

26. (Amended) A cultured tobacco cell transformed by the method according to Claim 1.

27. (Amended) A cultured tobacco BY2 cell transformed by the method according to Claim 1.

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30. (Amended) The repressor gene according to Claim 28 wherein said repressor gene is a barA gene.

31. (Amended) The repressor gene according to Claim 28 wherein said repressor gene contains a region comprising a nucleotide sequence shown under SEQ ID NO:1.

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32. (Amended) The repressor gene according to Claim 28 wherein said repressor gene contains a region coding for an amino acid sequence shown under SEQ ID NO:2.

35. (Amended) The modified promoter according to Claim 33, wherein a nucleotide sequence of said operator is BARE-1, BARE-2 or BARE-3.

36. (Amended) The modified promoter according to Claim 33, wherein the nucleotide sequence of said operator contains a region comprising a nucleotide sequence shown under SEQ ID NO:3.

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37. (Amended) The modified promoter according to Claim 33, wherein said operator is disposed, together with the TATA box of said plant promoter, in a manner shown under any of SEQ ID NO:4 through SEQ ID NO:7.